GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 18, 2002, 10:41:48; Search time 21 Seconds Run on:

(without alignments) 2681.350 Million cell updates/sec

US-09-802-668-105 Perfect score:

1 GTGPEFPGSRPALGPLSYRE......RKKKKKKKKKKKKKKKRRAAA 586 **BLOSUM62** Scoring table: Sednence:

Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:\* pir2:\* pir3:\* PIR 71:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		5HT3 receptor subu		nicotinio acotulat							nicotinic acetylch	nicotinic acetylch		nicotinic acetvlch									nicotinic acetylch	-	nicotinic acetylch	nicotinic acetylch		nicotinic acetylch				nicotinic acetylch nicotinic acetylch
SUMMARIES		1																															
SUM		150170	11001	S41757	A33523	ACCH2N	516333	ACCHAN	206802	01000	THO174	*/1010	210000	A26456	A39218	T09289	I38056	A55382	JC4021	A24572	A53956	A55972	A25338	260580	20000	100000	30/22/	B3/014	17471	ACHUA7	ACCH4N	JN0113	S14703
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	Length		7 9	487	464	528	466	491	462	454	503	0 0	7 0	070	0 / 4	494	423	479	627	499	503	455	501	495	105	1 0	2 5	7 0	0 (0	200	622	502	459
of	Query	24 5		C. 47	٠	14.5	14.5	4	4							٠	٠	٠				•	ω,		ω,	~			•	٠	٠	13.5	
	Score	764	764	٦.	407.0	452	450.5	448.5	446.5	441	441	440	436.5	435.5	; -	400	432	432	432		429.5	$\sim$		427.5	~	426.5	4	425		677	473	42	420.5
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nicotinic acctual ch	nicotinic acetylch	nicolinic acetylch	nypotnetical prote	alpha / neuronal n	nicolinic acetylch	nicotinic acetylch	nicotinic receptor	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	alpha-bungarotoxin	probable nicotinic	nicotinic acetylch	nicotinic acetylch	Diochtoto carried	nicotinic acetylch	macarina aceryical
A40110	S51116	T19622	602259	513873	A37040	T01378	0.0800	325721	A57175	TH0173	00000	76606	25/048	ACFFIN	B35721	S13875	
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511	455	560	502	501	502	502	521	452	505	51.	517	7 7 7	, ,	170	495	517	
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13	13	13	13	13	13.2	13	13	13	13	13	7	5	1	7	12	12.	
420.5	416	416	415	412.5	412.5	410	410	409	408	405	405	402 5	307 5		397	395.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	4.3		44	45	

## ALIGNMENTS

	12.2
	•
	Subuni +
-	receptor
SULT 8179	T3 F

5HT3 receptor subunit - rat (fragment) C;Species: Rattus sp. (rat) C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999

C.Accession: 158179
R.Isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Neuroreport 5, 121-124, 1993

A/Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit. A/Reference number: 158179; MUID:94154206
A/Reference number: 158179; MUID:94154206
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-462 <RES>
A/Cross-references: EMBL:001227; NID:9402245; PIDN:AAA52182.1; PID:9402246
C/Superfamily: acetylcholine receptor

12; 24.5%; Score 764; DB 2; Length 462; 37.6%; Pred. No. 1.3e-52; tive 88; Mismatches 142; Indels Matches 170; Conservative Query Match Best Local Similarity

64 RKPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 123 124 TKMSNAAKNLWLPDIFIIELMDVDKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFP 183 :| ||| : || |:| | |||:|:|: :|::::| | : ||:| |||: ::|
30 KKGVRPVRDWRKPILVSIDVIMYAILNVDEKNQVLITXIMYRQFWTDEFLQWTPEDFDNV 89 q ŏ

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184 FDQQNCTLTFSSFLYTVDSMLLDMEKEVW---EITDASRNILQTHGEWELLGLSKATAKL 240 a

241 S-RGGNLYDQIVFYVAIRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 299 ò

300 LGYNVFLIAMSDLLPTSG--TPLIGVYFALCLSLANGSLLETIFITHLLHVATTOPPPLP 357 266 LGYSVELIIVSDFLPATAIRTPLIGVYEVVCMALLVISLAETIFIVQLVHKQDLQ-RPVP 324 ò

358 RWLHSLLLH-----C--NSPGRCCPTAPQKENK-----GPGLTPTHLPGVKEPEVSA-- 402

325 DWLRHLVLDRIAWLLCLGEOPMAHRPPATFOANKTDDCSAMGNHCSHVGSPQDLEKTSRS 384 403 --GOMPGPAEAELTGGSEWTRAOREHEAOKOHSVEL------WLOFSHAMDAMLFR 450 q ò